

```

Db 61 IQPGMRLALGKGLNIDCLHBEVYGRDKCYTEDIIVLQDTRKYTSRHFRIQ 120
Qy 121 ELGHGSRVANYIEDLSNGTVPNKEIIGKRTLPITNNATIALSTNNVPPSDLSVD 180
Db 121 ELGHGSRVANYIEDLSNGTVPNKEIIGKRTLPITNNATIALSTNNVPPSDLSVD 180
Qy 181 QTIYPDPIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRFKNTSSNEHPIS 240
Db 181 QTIYPDPIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRFKNTSSNEHPIS 240
Qy 241 VDTREILKGLDHPICIKIENPPOSEDPYIIVLEMGSELPRVNVSTRLEPILAKYF 300
Db 241 VDTREILKGLDHPICIKIENPPOSEDPYIIVLEMGSELPRVNVSTRLEPILAKYF 300
Qy 301 YQMLAVOYLHNGVYIHRDLKPEVNLSTSESCCIKITDPCGSKILGTSILMRTLCGTP 360
Db 301 YQMLAVOYLHNGVYIHRDLKPEVNLSTSESCCIKITDPCGSKILGTSILMRTLCGTP 360
Qy 361 TYLAPEVLTAGTGYSSAVDCMSLGVILPVCLCGYPPFSQNSNIPLNQIABGKTYI 420
Db 361 TYLAPEVLTAGTGYSSAVDCMSLGVILPVCLCGYPPFSQNSNIPLNQIABGKTYI 420
Qy 421 AAAMRVSSQAPDLVKNLLVDPBQRLTTKQALSHPMLODSSMGTVERLMTGVDTHTMP 480
Db 421 AAAMRVSSQAPDLVKNLLVDPBQRLTTKQALSHPMLODSSMGTVERLMTGVDTHTMP 480
Qy 481 PIKNIIRKRGHEMDODASTSSCSSEILPITSABKRAK 517
Db 481 PIKNIIRKRGHEMDODASTSSCSSEILPITSABKRAK 517

RESULT 2
Q98TWO PRELIMINARY PRT: 517 AA.
ID Q98TWO
AC Q98TWO
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein kinase Cdel.
GN Name=Cdel;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OC NCBI_TaxID=8335;
RX NCBI_TaxID=8335;
RN 1)
RS SEQUENCE FROM N.A.
RA Matsui T., Nakaniishi M., Takisawa H.;
RA Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF26574; AAG59884.1;
DR HSBP; 096017; IGCC.
DR CO; GO:0005524; P-ATP binding; IEA.
DR CO; GO:0004674; P-protein serine/threonine kinase activity; IEA.
DR CO; GO:0016740; P:transferase activity; IEA.
DR CO; GO:0006668; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR00253; FHA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR00719; Prot Kinase.
DR InterPro; IPR002290; Ser-Thr kinase.
DR InterPro; IPR008271; Ser-Thr_pkin_AS.
DR InterPro; IPR008984; SMD_FHA.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00240; FHA; 1.
DR SMART; SM00240; S_TKc; 1.
DR PROSITE; PS50006; FHA_DOMAIN; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR AP- binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 517 AA; 58310 MW; 401A3235AA0BDCBB CRC64;

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Query Match 99.7%; Score 2704; DB 2; Length 517;
Best Local Similarity 99.8%; Pred. No. 4,56-164;
Matches 516; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MMSRDTKTESQOSQCTSSSSSSSAPQSYQSQSSSGTSLSDTPVPVQDLASIPDPRIED 60
Db 1 MMSRDTKTESQOSQCTSSSSSSSAPQSYQSQSSSGTSLSDTPVPVQDLASIPDPRIED 60
Qy 61 IQPGMRLALGKGLNIDCLHBEVYGRDKCYTEDIIVLQDTRKYTSRHFRIQ 120
Db 61 IQPGMRLALGKGLNIDCLHBEVYGRDKCYTEDIIVLQDTRKYTSRHFRIQ 120
Qy 121 ELGHGSRVANYIEDLSNGTVPNKEIIGKRTLPITNNATIALSTNNVPPSDLSVD 180
Db 121 ELGHGSRVANYIEDLSNGTVPNKEIIGKRTLPITNNATIALSTNNVPPSDLSVD 180
Qy 181 QTIYPDPIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRFKNTSSNEHPIS 240
Db 181 QTIYPDPIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRFKNTSSNEHPIS 240
Qy 241 VDTREILKGLDHPICIKIENPPOSEDPYIIVLEMGSELPRVNVSTRLEPILAKYF 300
Db 241 VDTREILKGLDHPICIKIENPPOSEDPYIIVLEMGSELPRVNVSTRLEPILAKYF 300
Qy 301 YQMLAVOYLHNGVYIHRDLKPEVNLSTSESCCIKITDPCGSKILGTSILMRTLCGTP 360
Db 301 YQMLAVOYLHNGVYIHRDLKPEVNLSTSESCCIKITDPCGSKILGTSILMRTLCGTP 360
Qy 361 TYLAPEVLTAGTGYSSAVDCMSLGVILPVCLCGYPPFSQNSNIPLNQIABGKTYI 420
Db 361 TYLAPEVLTAGTGYSSAVDCMSLGVILPVCLCGYPPFSQNSNIPLNQIABGKTYI 420
Qy 421 AAAMRVSSQAPDLVKNLLVDPBQRLTTKQALSHPMLODSSMGTVERLMTGVDTHTMP 480
Db 421 AAAMRVSSQAPDLVKNLLVDPBQRLTTKQALSHPMLODSSMGTVERLMTGVDTHTMP 480
Qy 481 PIKNIIRKRGHEMDODASTSSCSSEILPITSABKRAK 517
Db 481 PIKNIIRKRGHEMDODASTSSCSSEILPITSABKRAK 517

RESULT 3
CHK2 HUMAN STANDARD: PRT: 543 AA.
ID CHK2 HUMAN
AC Q96017; Q9UGP0; Q9UGP1;
DT 30-MAY-2000 (Ref. 39, Created)
DT 30-MAY-2000 (Ref. 39, Last sequence update)
DT 25-OCT-2004 (Ref. 45, Last annotation update)
DE Serine/threonine-protein kinase Chk2 (BC 2.7.1.37) (Cdel).
GN Name=CHK2; Synonyms=CHK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RX NCBI_TaxID=9606;
RN 1)
RS SEQUENCE FROM N.A.
RA MEDLINE=99108191; PubMed=9889122; DOI=10.1016/S0960-9822(99)80041-4;
RA Bleasins A., van de Weyer I., Laue M.C., Luyten W.R.M.L., Parker A.B.,
RA McCowan C.H.;
RA "A human homologue of the checkpoint kinase Cdel directly inhibits
RA Cdc25 phosphatase."
RT Curr. Biol. 9:1-10(1999).
RL 1)
RN 2)
RS SEQUENCE FROM N.A.
RA MEDLINE=99055399; PubMed=9836640; DOI=10.1126/science.282.5395.1893;
RA Matsuno S., Huang M., Ellledge S.J.;
RA "Linkage of ATM to cell cycle regulation by the Chk2 protein kinase."
RL Science 282:1893-1897(1998).
RN 1)
RN 2)
RS SEQUENCE FROM N.A.
RA MEDLINE=99192255; PubMed=10097108; DOI=10.1073/pnas.96.7.3745;
RA Brown A.L., Lee C.-H., Schwarz J.K., Mitiku N., Plimica-Worms H.,

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RA Chung J.H.;
 RA "A human Cdc1-related kinase that functions downstream of ATM protein
 RT in the cellular response to DNA damage.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:3745-3750(1999).
 RP [6]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Colon carcinoma;
 RA Shao R.-G., Zhang H., Yu Q., Pommler Y.;
 RT "Chk2/hmcd2 cell cycle checkpoint protein kinase from human colon
 carcinoma HT29 cells: regulation by autophosphorylation and DNA-
 RT dependent protein kinase and inhibition by cell cycle regulatory
 RT drugs.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RP [5]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=2005165; PubMed=10591208; DOI=10.1038/99003;
 RA Dunham I., Hunt A.R., Collins J.E., Brunelle R., Beare D.M.,
 RA Camp M., Sank L.J., Alencough R., Almeida J.P., Babbage A.K.,
 RA Bagnall C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burdill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.B., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corry N.R., Coville G.J., Cox A.V., Davis J., Dawson B.,
 RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Grahan R.V., Griffiths W.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.V., Ho S., Holmes S.,
 RA Hall S.B., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird J.R., Langford C.P., Leverisa M.A., Lloyd C., Lloyd D.M.,
 RA Martin I.D., Mashregi-Mohammadi M., Matthews L.H., Mccann O.T.,
 RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Mcclay C.N., Pavitt R., Pearce A.V., Pearson D., Phillips B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sena H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson R., Wilmer T.E., Wilmington L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shmizu N.,
 RA Wilmshus S., Kawaaki K., Sasaki T., Asakawa S., Kudo J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsunuma S.,
 RA Roe B.A., Chen P., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Doorman A., Pang P., Pu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Lon P., Malsbendy S., Ngan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shull S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chisose S., Murray J., Miller N., Mix P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinde K., Kemp K., Latreille P., Layman D., Ozersky P., Roulifson T.,
 RA Scheer P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
 RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salter S.,
 RA Budart M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
 RA Bedalov L., Kim U.J., Shizuya H., Simon M.L., Dunham J.P.,
 RA Peyrard M., Keda D., Seroussi B., Pransoni I., Tapia J., Bruder C.E.,
 RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
 RA Khan A.S., Lane L., Tilihan Y., Wright H.;
 RT "The DNA sequence of human chromosome 22.";
 RL Nature 402:489-495(1999).
 RP [6]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Muscle;
 RA MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Greuse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow R.H., Scheffer C.F., Bhat N.G.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Datschenko L., Marsina K., Farmer A.R., Rubin G.M., Hong L.,
 RA Stedman M., Soares M.B., Bonaldi M.F., Casavini T.L., Scheetz T.B.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carinici P., Prange C.,
 RA Rata S.S., Loguolano N.A., Peters G.J., Abrahamson R.D., Mullaly S.H.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarnatieri P.H.,
 RA Richards S., Worley K.C., McKernan K.J., Malek J.A., Guarnatieri P.H.,
 RA Richards S., Worley K.C., McKernan K.J., Malek J.A., Guarnatieri P.H.,

RA Villalón D.R., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Paiting J., Helton B., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N.,
 RA Butlerfield Y.S.N., Krzywicki M.J., Skolnik U., Smalley D.B.,
 RA Bucherich A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [7]
 RP VARIANT THR-157, AND VARIANT COLON CANCER TRP-145.
 RA MEDLINE=20085462; PubMed=10617473; DOI=10.1126/science.286.5449.2528;
 RA Bell D.W., Varley J.M., Szlylo T.B., Kang D.H., Wahner D.C.R.,
 RA Shannon K.E., Lubratovich M., Veralis S.J., Jasebacher K.J.,
 RA Frenkel J.F., Birch J.M., Li P.P., Garber J.E., Haber D.A.;
 RT "Heterozygous germ line hCHK2 mutations in Li-Fraumeni syndrome.";
 RL Science 286:2528-2531(1999).
 RP [8]
 RP VARIANT THR-157.
 RA PubMed=11461078; DOI=10.1054/bjoc.2001.1858;
 RA Allinen M., Hunko P., Mäntylä S., Launonen V., Winqvist R.;
 RT "Mutation analysis of the CHK2 gene in families with hereditary breast
 RT cancer.";
 RL Br. J. Cancer 85:209-212(2001).
 RP [9]
 RP VARIANTS OSTROCARCINOMA SER-17 AND LEU-85.
 RA PubMed=11746983; DOI=10.1002/gcc.1207;
 RA Miller C.W., Ikezoe T., Krug U., Hofmann W.K., Tavor S., Vegesna V.,
 RA Takaaki K., Takeuchi S., Koefler H.P.;
 RT "Mutations of the CHK2 gene are found in some osteosarcomas, but are
 RT rare in breast, lung, and ovarian tumors.";
 RL Genes Chromosomes Cancer 33:17-21(2002).
 RP [10]
 RP VARIANTS PROSTATE CANCER LYS-64, PRO-145, ARG-167, CYS-180, HIS-180;
 RP CYS-181, HIS-181, LYS-239, PHE-251, HIS-318, PRO-323; CYS-327 AND
 RP LYS-476, AND VARIANT THR-157.
 RA PubMed=12531788;
 RA Dong X., Wang L., Taniguchi K., Wang X., Cunningham J.M.,
 RA McConnell S.K., Qian C., Marks A.F., Sleser S.L., Peterson B.J.,
 RA Smith D.J., Cheville J.C., Blute M.L., Jacobsen J.J., Schaid D.J.,
 RA Tindall D.J.;
 RT "Mutations in CHK2 associated with prostate cancer risk.";
 RL Am. J. Hum. Genet. 72:270-280(2003).
 RP [11]
 RP FUNCTION: Controls cell cycle checkpoint. May participate in
 RP transduction of the DNA damage and replication stress signals.
 RP Inhibits CDC25C phosphatase by phosphorylating it on Ser-216,
 RP preventing the entry into mitosis. May have a role in meiosis as
 RP well.
 RP -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 RP -1- ENZYME REGULATION: Kinase activity is up-regulated by
 RP autophosphorylation. Rapidly phosphorylated in response to DNA
 RP damage and to replication block.
 RP -1- SUBCELLULAR LOCATION: Nuclear.
 RP -1- TISSUE SPECIFICITY: High expression is found in testis, spleen,
 RP colon and peripheral blood leukocytes. Low expression is found in
 RP other tissues.
 RP -1- DISEASE: Defects in CHK2 are associated with Li-Fraumeni syndrome
 RP (LFS) [MIM:151623], a highly penetrant familial cancer phenotype
 RP usually associated with inherited mutations in p53/TP53.
 RP -1- DISEASE: Defects in CHK2 are found in some patients with prostate
 RP cancer (Cap) [MIM:176807].
 RP -1- DISEASE: Defects in CHK2 are found in some patients with
 RP osteosarcoma (OSRC) [MIM:259500].
 RP -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. CDS1
 RP subfamily.
 RP -1- SIMILARITY: Contains 1 PWA domain.
 RP This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 RP between the Swiss Institute of Bioinformatics and the EMBL outstation
 RP at the European Bioinformatics Institute. There are no restrictions on its
 RP use by non-profit institutions as long as its content is in no way
 RP modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.fdb-sib.ch/announce/> or send an email to license@fdb-sib.ch).

DR EMBL; AJ131197; CA10319.1; -
 DR EMBL; AF086904; AAC83693.1; -
 DR EMBL; AF096379; AAD11784.1; -
 DR EMBL; AF174135; AAD48504.1; -
 DR EMBL; AL117130; CAB63923.1; -
 DR EMBL; AL121825; CAB63922.1; -
 DR EMBL; BC004207; AAH04207.1; -
 DR PDB; 1GNC; X-ray; A/D/G/J=64-212.
 DR Genew; HGNC; 16627; CHK2.
 DR H-INVD; HIX016341; -
 DR Reactome; 096017; -
 DR MIM; 604373; -
 DR MIM; 151623; -
 DR MIM; 176807; -
 DR MIM; 259500; -
 DR CO; GO:0005634; C:nucleus, NAS.
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; TAS.
 DR GO; GO:0000077; P:DNA damage response, signal transduction re.; TAS.
 DR GO; GO:0006974; P:response to DNA damage stimulus; TAS.
 DR InterPro; IPR000253; FHA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.

Query Match 61.0%; Score 1655.5; DB 1; Length 543;
 Best Local Similarity 59.0%; Pred. No. 2.9e-97;

Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;

QY 2 MSRTKTSQ-----OSGTSSSSSSSAP-OSYSSSSSGTL 37
 1 MSRSDEVAQSGHSGSACSPHGSVYSGSSSSGSISSSTSTPNSSQSSHSSGTL 60
 QY 36 SLSLTPVVDLASI-----PDPPIDEIPQPMKRLALGKPLNDCLEHYVGRDK 92
 61 SLELVSTQELYSIEDQEPEDQEEETPAFARLALDQFPAHLECVANDNWFGRDSS 120
 QY 93 CDYTPIDVLANOTDRKTYSRKPRIPQELGHSRVANIEDLSGNGTVPNKEIYCKRT 152
 121 CERDEDEPLKRTDKRYTSKKHFRIFREVPKNSYAYIEDSGNGTFVTELVGGR 180
 QY 153 LPLTNNAETALSLPTNKVFVSDLSVDQITYPDPIDKTYMRSPIGSGACGVTLAPQK 212
 181 RPLNNSETALSLSNKVFVFDLTVDDQSVFPLALDSTINRKTLSGACGVTLAPK 240
 QY 213 SVCKVAVVTKISKRPKMTSNEHP-ISVDTEIILKLDHPCLIKINFPDSDFYI 271
 241 KTCCKVALTKISKRPALGSARADPALMVEIEILKLNHPCLIKINFPDABD-VYI 299
 QY 272 VLEMEGSELPRVNVSTRLEPIAKLYFYQMLAVOYLHNGVIRHDLKPEVLLSSTS 331
 300 VLEMEGSELPRVNVSTRLEPIAKLYFYQMLAVOYLHNGVIRHDLKPEVLLSSTS 359
 QY 332 BECCIKITDPGSKILGISTLMRTLCGPTTLAERYANTAGTGYSAVDCMSLGYILFV 391
 360 EGCCLKITDPGSKILGISTLMRTLCGPTTLAERYANTAGTGYSAVDCMSLGYILFV 419
 QY 392 CLCGTPPPEBONSNIPLANOIABGKTYTYIAAMRVNSBOAPDLVKNLAVDDEBOLTLTKQ 451
 420 CLSGTPPPEBKHQVSLKQITSGKYNFIPVMAVSEKALDVKGLVVDPAARTTEE 479
 QY 452 ALSEPLAODSMWHTVERLVNGVDHTMPP---IKKIIKRGHEMDQDASTSS-----C 503
 480 ALRHWLQDEBKHQVGLSLSEHNSIALPOVLAQPSSTSHKRPBESAGASTTKRPAVC 539
 DB 504 SEIL 507
 DB 540 AAVL 543

RESULT 4
 098019

ID 098019 PRELIMINARY, PRT, 545 AA.

AC 098019
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE Checkpoint kinase Chk2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID:10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TTSURE-Thymus;
 RX MEDLINE:9361938; PubMed:10435585; DOI:10.1038/gj.onc.1202925;
 RA Chaturvedi P., Eng W.K., Zhu Y., Mattern M.R., Mishra R., Hurtle M.R.,
 RA Zhang X., Annan R.S., Lu Q., Faucette L.F., Scott G.F., Li X.,
 RA Carr S.A., Johnson R.K., Winkler J.D., Zhou B.B.;
 RT "Mammalian Chk2 is a downstream effector of the ATM-dependent DNA
 RT damage checkpoint pathway."
 RL Oncogene 18:4047-4054(1999).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AF134054; AAD55890.1; -
 DR HSP; 096017; 1GNC.

DR CO; GO:0005524; F:ATP binding; IEA.
 DR CO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
 DR CO; GO:0016740; P:transferase activity; IEA.
 DR CO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000253; FHA.
 DR InterPro; IPR001109; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR008271; Ser_Thr_kinase.
 DR InterPro; IPR008984; SMAD_FHA.
 DR Pfam; PF00438; FHA_1.
 DR Pfam; PF00693; PKinase; 1.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR SMART; SM00240; FHA_1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS50006; FHA DOMAIN; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; kinase; serine/threonine-protein kinase; Transferase.
 SO SEQUENCE 545 AA; 60930 MW; C8332AD08608873 CRC64;

Query Match 60.6%; Score 1644.5; DB 2; Length 545;
 Best Local Similarity 63.0%; Pred. No. 1.5e-96;
 Matches 327; Conservative 69; Mismatches 108; Indels 15; Gaps 7;

QY 3 SRDTKTSQ-----OSGTSSSSSSSAP-OSYSSSSSGTSLDTPVVDLASEPDE 56
 28 SSGSQTPSQDHLDSQYQASSSSTSTVPSGSSSSSGTSLSELYSTQELQSIPEDE 87
 QY 57 IBDITFQPMGRMALGKPLNDCLEHYVGRDKCDYTPIDVLANOTDRKTYSRKPR 116
 88 PEPGFTPAFARLALDQFPAHLECVANDNWFGRKSEYCPDGLKRTKRYTSKRP 147
 QY 117 RIFQSLGHSRVANIEDLSGNGTVPNKEIYCKRTPLTNNAETALSLPTNKVFVPSDL 176
 148 RIFREKSPKNCYIYLBHSGNGTFVTEILGKQKCPILSNNSIALSLKRNKVFVFDL 207
 QY 177 SYDDQITYPKIDKTYMRSPIGSGACGVTLAOKSVCKKVAVKIISKRPKMTSNE 235
 208 TYDDQSVFPEKLEADTYISKTLGSGACGVTLAOKSVCKKVAVKIISKRPKMTSNE 267
 QY 236 EHPISVDTEIILKLDHPCLIKINFPDSDFYIYVLEMEGSELPRVNVSTRLEPI 295
 268 DTAPSVETIEIILKLDHPCLIKINFPDABD-VYIYVLEMEGSELPRVNVSTRLEPI 326
 QY 296 AKLYFYQMLAVOYLHNGVIRHDLKPEVLLSSTSBECCIKITDPGSKILGISTLMRT 355
 327 CLKLYFYQMLAVOYLHNGVIRHDLKPEVLLSSTSBECCIKITDPGSKILGISTLMRT 386
 QY 356 LCGTPTTLAERYANTAGTGYSAVDCMSLGYILFVCLCGTPPPEBONSNIPLANOIABG 415